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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 09:48:28 ; Search time 2772.05 Seconds  
(without alignments)  
11181.073 Million cell updates/sec

Title: US-09-922-895-2

Perfect score: 1065

Sequence: 1 ATGACACCTCCTAGATAC.....CGGAACCTCTATTGTGTTT 1065

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
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25: em\_pl:\*  
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27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
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31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vtl:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1065	100.0	1065	6 AR164119	AR164119 Sequence
2	1065	100.0	1065	6 AX030929	AX030929 Sequence
3	1065	100.0	1068	9 AF026535	AF026535 Homo sapi
4	1065	100.0	1201	9 HSU28654	HSU28654 Human eosin
5	1065	100.0	1717	6 AX334894	AX334894 Sequence
6	1065	100.0	1717	6 HSU051241	HSU051241 Human eosin
7	1065	100.0	1915	6 BD006761	BD006761 Chemokine
8	1065	100.0	5791	9 AF247361	AF247361 Homo sapi
9	1065	100.0	197279	9 AC104439	AC104439 Homo sapi
10	1065	100.0	220965	2 HSA312688	HSA312688 Homo sapi
11	1061.8	99.7	1068	6 AX280851	AX280851 Sequence
12	1061.8	99.7	1689	6 AX323054	AX323054 Sequence
13	1061.8	99.7	1689	6 HSU49727	HSU49727 Human C-C
14	1060.2	99.5	1068	9 AB023887	AB023887 Homo sapi
15	980.2	92.0	1068	9 CAY13775	CAY13775 Cercopithe
16	977.7	91.7	1068	9 AY065647	AY065647 Macaca fa
17	975.4	91.6	1068	9 AY065646	AY065646 Macaca fa
18	975.4	91.6	1068	9 MMY13776	MMY13776 Macaca mla
19	975.4	91.6	1108	9 AF291668	AF291668 Macaca fa
20	972.2	91.3	1068	9 AF017283	AF017283 Macaca mu
21	713.3	66.9	7201	6 AX345239	AX345239 Sequence
22	700.2	65.7	1119	4 AF266468	AF266468 Ovis arie
23	663.2	62.3	1440	10 MMU28406	MMU28406 Mus muscu
24	661.6	62.1	1080	10 AY049018	AY049018 Mus muscu
25	660	62.0	1185	10 MMU29677	MMU29677 Mus muscu
26	652	61.2	1315	10 RNRPCR3	RNRPCR3 Rattus norv
27	650.4	61.1	1080	10 AF003954	AF003954 Rattus no
28	637.8	59.9	7201	6 AX345238	AX345238 Sequence
29	636.2	59.7	1077	10 AF060698	AF060698 Cavia por
30	540.8	50.8	1495	9 HUMCCCKR1A	HUMCCCKR1A Homo sapi
31	540.8	50.8	1609	6 E13385	E13385 CDNA encod1
32	540.8	50.8	2156	6 I58541	I58541 Sequence 1
33	540.8	50.8	2156	6 HUMRANES	HUMRANES Homo sapien
34	540.8	50.8	2214	9 HUMHMI45	HUMHMI45 Human mRNa
35	540.8	50.8	197279	9 AC104439	AC104439 Homo sapi
36	540.8	50.8	220965	2 HSA312688	HSA312688 Homo sapi
37	524.6	49.3	1068	4 AF127528	AF127528 Callithr1
38	522	49.0	1068	4 AF127527	AF127527 Oryctolag
39	507.2	47.6	1068	9 AF017282	AF017282 Macaca mu
40	487.2	45.7	1068	10 AF119381	AF119381 Rattus no
41	487.2	45.7	1544	6 E13732	E13732 CDNA encod1
42	480.8	45.1	1748	10 MMU28404	MMU28404 Mus muscu
43	479.2	45.0	1068	10 MMU29678	MMU29678 Mus muscu
44	479.2	45.0	1703	10 BC011092	BC011092 Mus muscu
45	403.6	37.9	1371	10 MMU28405	MMU28405 Mus muscu

#### ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	2 from patent US 6271347.	DNA	linear	PAT 17-OCT-2001
AR164119	AR164119	Sequence	2 from patent US 6271347.	DNA	linear	PAT 17-OCT-2001
DEFINITION	AR164119	Sequence	2 from patent US 6271347.	DNA	linear	PAT 17-OCT-2001
ACCESSION	AR164119	Sequence	2 from patent US 6271347.	DNA	linear	PAT 17-OCT-2001
VERSION	AR164119.1	GI:16235065				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (Bases 1 to 1065)					
AUTHORS	Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.					
TITLE	Eosinophil eotaxin receptor					
JOURNAL	Patent: US 6271347-A 2 07-AUG-2001;					
FEATURES	Location/Qualifiers					



Db	541	ACTCTTTGGCACTGCTCTTTTACCCAGAGGATATACAGTATATAGCTGGAGGCAATTTCCACT	600
Qy	601	CTGGAATGACCATCTTCTGCTGCTGCTCCCTGCTGCTATATAGGCAATCTGCTACACA	660
Db	601	CTGGAATGACCATCTTCTGCTGCTGCTCCCTGCTGCTATATAGGCAATCTGCTACACA	660
Qy	661	GGATTCATCAAAACGCGTGGAGGTGCCAGTAAAAAAGTACAAAGGCCATCCGGCTC	720
Db	661	GGATTCATCAAAACGCGTGGAGGTGCCAGTAAAAAAGTACAAAGGCCATCCGGCTC	720
Qy	721	ATTTTGTGCATCATGGCGGTGTTTTTTCATTTTCTGACACCCCTACAAATGTGGCTATCCT	780
Db	721	ATTTTGTGCATCATGGCGGTGTTTTTTCATTTTCTGACACCCCTACAAATGTGGCTATCCT	780
Qy	781	CTCTCTTCCTATCAATCCATCTTATTTGGAAATACAGTATAGGGGAGCAAGCATCTGGAC	840
Db	781	CTCTCTTCCTATCAATCCATCTTATTTGGAAATACAGTATAGGGGAGCAAGCATCTGGAC	840
Qy	841	CTGGTCATGCTGGAGAGAGGTGATCCCTACCTCCACTGTCGATGTAACCCGGTGATC	900
Db	841	CTGGTCATGCTGGAGAGAGGTGATCCCTACCTCCACTGTCGATGTAACCCGGTGATC	900
Qy	901	TACGCTTTGTTGGAGAGAGTTCGCGAAGTACCTGGCCACTTTCTTCCACAGGCACTTG	960
Db	901	TACGCTTTGTTGGAGAGAGTTCGCGAAGTACCTGGCCACTTTCTTCCACAGGCACTTG	960
Qy	961	CTCATGCACTGGGAGATATACATCCATTCCTCTAGTGAAGCGGAAACACAGC	1020
Db	961	CTCATGCACTGGGAGATATACATCCATTCCTCTAGTGAAGCGGAAACACAGC	1020
Qy	1021	TCTGTCTCTCCATCCACAGCAGACCGGAATCTCTATTTGTGTT	1065
Db	1021	TCTGTCTCTCCATCCACAGCAGACCGGAATCTCTATTTGTGTT	1065
RESULT 3			
LOCUS	AF026535	1068 bp	mRNA linear
DEFINITION	Homo sapiens chemokine receptor (CCR3) mRNA, complete cds.		
ACCESSION	AF026535		
VERSION	AF026535.1	GI:2582565	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiindae; Homo.		
AUTHORS	1 (bases 1 to 1068)		
TITLE	Xiao L., Weiss S., Oari S., Rudolph D., Hodge T. and Lal R.		
JOURNAL	Partial resistance to infection by syncytium-inducing primary HIV-1 in exposed uninfected individuals homozygous for CCR5 32bp deletion		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1068)		
TITLE	Qari S.		
JOURNAL	Direct Submission		
AUTHORS	Submitted (24-SEP-1997)		
TITLE	Retrovirus Diseases Branch, Centers for Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA		
JOURNAL	30333, USA		
FEATURES			
source	Location/Qualifiers		
	1..1068		
	/organism="Homo sapiens"		
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	/chromosome="3"		
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	/gene="CCR3"		
CDS	1..1068		
	/codon_start=1		
	/product="chemokine receptor"		
	/protein_id="AA82589.1"		
	/translation="MTSLDVTETEGTSTYYDVLGCEKADTRALMAQFVPLVSLV		
	FTVLGLGVMVVMILIRYRIRIRMTNITLNLNISDLFLVTLPIFIHYRGNNWVG		

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 Db 901 TACCCCTTTGTTGGAGAGGTTCCGGAAGTACCTGCGCCACTTCTCCACAGGCACTTG 960  
 Oy 961 CTCATGACCGGGGACAGATCATCCATTCCTTCGTAGTGAGAGCGGAAAGACAGC 1020  
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 Db 961 CTCATGACCGGGGACAGATCATCCATTCCTTCGTAGTGAGAGCGGAAAGACAGC 1020  
 Oy 1021 TCTGTCTCTCCATCCACAGCAGACCGGAACTCTCTATTGTGTTT 1065  
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 Db 1021 TCTGTCTCTCCATCCACAGCAGACCGGAACTCTCTATTGTGTTT 1065

RESULT 4  
 HSU28694 1201 bp mRNA linear PRI 16-MAY-1996  
 LOCUS Human eosinophil CC chemokine receptor 3 mRNA, complete cds.  
 DEFINITION U28694  
 ACCESSION U28694  
 VERSION U28694.1 GI:1199579  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
 AUTHORS Combadiere,C., Ahuja,S.K. and Murphy,P.M.  
 TITLE Cloning and functional expression of a human eosinophil CC chemokine receptor  
 JOURNAL J. Biol. Chem. 270 (28), 16491-16494 (1995)  
 MEDLINE 95348056  
 PUBMED 7622448  
 REFERENCE  
 AUTHORS Combadiere,C.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-JUN-1995) Christophe Combadiere, NIAID, National Institutes of Health, Building 10, Room 11N11, Bethesda, MD 20892, USA  
 REFERENCE  
 AUTHORS 3 (bases 1 to 1201)  
 TITLE Cloning and functional expression of a human eosinophil CC chemokine receptor  
 JOURNAL J. Biol. Chem. 271 (18), 11034 (1996)  
 MEDLINE 96210048  
 PUBMED 8631926  
 COMMENT On Feb 22, 1996 this sequence version replaced gi:881569.  
 FEATURES  
 source Location/Qualifiers  
 1. 1201  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /cell\_type="eosinophil"  
 32..1099  
 /codon\_start=1  
 /product="CC chemokine receptor 3"  
 /protein\_id="AAC50469.1"  
 /db\_xref="GI:1199580"  
 /translation="MTSLDYVEFTGTSYVDVGLCKEADTRALMAQFVPLVSLV  
 FTVGLGNVAVVMIILIKYRRLMTNIVILNLASDLPLVLPFIHVRGNWVG  
 HMKCKLSEFHYGLYSEIFLIITIDRYLAIVHAFVLRATVFGVTSIVTGL  
 AVLAALPERIFYETBELFEETCSALYPEDIVYSRHFRLMTIFCLVPLVMAIC  
 YGIKITLRCPSSKELFKRAIRLIFVIMAFEFIMRYNAIILSSOSTLFGDCRS  
 KHLDIAMLYTEVIAVSHCCMNPIYIVAFVERRRKYLIRHFPHRLMLHRLRYLPFLPSE  
 KLERSSVSPSTAEPELSTIV"

CDS  
 278 a 320 c 267 g 336 t  
 BASE COUNT  
 ORIGIN

Query Match 100.0%; Score 1065; DB 9; Length 1201;  
 Best local Similarity 100.0%; Pred No. 7.2e-277;  
 Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 61 GGCCTGCTGTGTGAAGAGCTGATACAGACAGTATGAGCCGACGTTGTGCCCGGCTG 120  
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 Db 92 GGCCTGCTGTGTGAAGAGCTGATACAGACAGTATGAGCCGACGTTGTGCCCGGCTG 121  
 Oy 121 TACTCCCTGTGTGTGCTGCTGAGGCGCTCTGAGGAGTGTGTGTGATGATCTTCATA 180  
 |||||  
 Db 152 TACTCCCTGTGTGTGCTGCTGAGGCGCTCTGAGGAGTGTGTGTGATGATCTTCATA 211  
 Oy 181 AAATACAGAGAGGCTCCCAATATGACCAATCTACTGCTCAACCTGGCCATTTGGGAC 240  
 |||||  
 Db 212 AAATACAGAGAGGCTCCCAATATGACCAATCTACTGCTCAACCTGGCCATTTGGGAC 271  
 Oy 241 CTGCTCTTCCCTGCTGACCTTCCATCTGATCATGATGAGGAGGAGCTTAACTGGGTT 300  
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 Db 272 CTGCTCTTCCCTGCTGACCTTCCATCTGATCATGATGAGGAGGAGCTTAACTGGGTT 331  
 Oy 301 TTGGCCATGGCATGTGTAAAGCTCTCTCAAGGTTTATACACAGAGCTTGTACAGGAG 360  
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 Db 332 TTGGCCATGGCATGTGTAAAGCTCTCTCAAGGTTTATACACAGAGCTTGTACAGGAG 391  
 Oy 361 ATCTTTTCAATATCCCTGCTGACCAATGACAGTACCTGGCCATTTGCTGTGTTT 420  
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 Db 392 ATCTTTTCAATATCCCTGCTGACCAATGACAGTACCTGGCCATTTGCTGTGTTT 451  
 Oy 421 GCCCTTGAGAGCCGGAGCTGTCACCTTTGTGTATCACCAGCATGCTGAGGCGCTG 480  
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 Db 452 GCCCTTGAGAGCCGGAGCTGTCACCTTTGTGTATCACCAGCATGCTGAGGCGCTG 511  
 Oy 481 GCACTGCTACAGAGCTCTTCTGTAATTTATCTTATGAGAGCTAAGAGTTGTTGAAGAG 540  
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 Db 512 GCACTGCTACAGAGCTCTTCTGTAATTTATCTTATGAGAGCTAAGAGTTGTTGAAGAG 571  
 Oy 541 ACCTTTGACAGTGTCTTTTACCCAGAGATACAGTATATGCTGGAGGCTTCCACACT 600  
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 Db 572 ACCTTTGACAGTGTCTTTTACCCAGAGATACAGTATATGCTGGAGGCTTCCACACT 631  
 Oy 601 CTGAGATGACATCTTCTGCTGCTTCTCCCTGCTGCTTATGAGCATCTCTACACA 660  
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 Db 632 CTGAGATGACATCTTCTGCTGCTTCTCCCTGCTGCTTATGAGCATCTCTACACA 691  
 Oy 661 GGATATCTCAAAACGCTGCTGAGGTGCCCCAGTAAAAAGTAAAGGCGCATCCGGCTC 720  
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 Db 692 GGATATCTCAAAACGCTGCTGAGGTGCCCCAGTAAAAAGTAAAGGCGCATCCGGCTC 751  
 Oy 721 ATTTTGTCTCAATGAGGCGGTGTTTTCATTTCTGAGACCTCAATGAGGCTATCTT 780  
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 Db 752 ATTTTGTCTCAATGAGGCGGTGTTTTCATTTCTGAGACCTCAATGAGGCTATCTT 811  
 Oy 781 CTCTCTTCTATCATTCATCTTATTTGGAATAGCTGTGAGGAGCAAGCATCTGGAC 840  
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 Db 812 CTCTCTTCTATCATTCATCTTATTTGGAATAGCTGTGAGGAGCAAGCATCTGGAC 871  
 Oy 841 CTGCTATGCTGTGACAGAGGTGATGCTCTACTCCCATGCTGCTATGAACCGGTGATC 900  
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 Db 872 CTGCTATGCTGTGACAGAGGTGATGCTCTACTCCCATGCTGCTATGAACCGGTGATC 931  
 Oy 901 TAGGCTTTGTTGGAAGAGTTCGGAAGTACTCGGACACTTCTCCACAGGCACTTG 960  
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 Db 932 TAGGCTTTGTTGGAAGAGTTCGGAAGTACTCGGACACTTCTCCACAGGCACTTG 991  
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 Db 992 CTCATGACCGTGGGAGATATCATCCATTCCTTCTAGTGAAGAGCTGGAAGAACACAGC 1051  
 Oy 1021 TCTGTCTCTCCATCCACAGCAGAGCGGAACTCTCTATTGTGTTT 1065  
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 Db 1052 TCTGTCTCTCCATCCACAGCAGAGCGGAACTCTCTATTGTGTTT 1096

RESULT 5  
 AX334894 1717 bp DNA linear PAT 09-JAN-2002  
 LOCUS AX334894  
 DEFINITION Sequence 5403 from Patent WO0194629.

ACCESSION AX334894  
VERSION AX334894.1 GI:18125613  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1  
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
Horligan, S., Soppet, D.R. and Weaver, Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
JOURNAL gene sets  
Patent: WO 0194629-A 5403 13-DEC-2001;  
FEATURES Avalon Pharmaceuticals (US)  
source 1. 1717  
Location/Qualifiers  
BASE COUNT 434 a 428 c 351 g 504 t  
ORIGIN  
Query Match 100.0%; Score 1065; DB 6; Length 1717;  
Best Local Similarity 100.0%; Pred. No. 7.5e-277;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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925 ATTTTGTGATCATGCGGGGTGTTTTTCATTTTCTGACACCCCTACAAATGTGCTATCTT 984  
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781 CTCTCTCTATCATATCCATCTTATTTGGAATGACTGTGACGGGAGCAAGCATCTGGAC 840  
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841 CTGTCATGCTGTGTCACAGAGGATGATCGGCTACTCCACTGTCGATGGAACCGGATGAC 900  
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1045 CTGTCATGCTGTGTCACAGAGGATGATCGGCTACTCCACTGTCGATGGAACCGGATGAC 1104  
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901 TAGCCCTTTGTTGGAGAGAGTCCGGAAGTACCTCGCCACTTCTCCACAGGACACTTG 960  
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1021 TCTGTCCTGCATCCACAGAGAGCGGGAACCTCTATTGTGTTT 1065  
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1225 TCTGTCCTGCATCCACAGAGAGCGGGAACCTCTATTGTGTTT 1269  
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RESULT 6  
HSU51241 1717 bp DNA linear PRI 09-OCT-1996  
LOCUS  
DEFINITION Human eosinophil eotaxin receptor (CMBR3) gene, complete cds.  
ACCESSION U51241  
VERSION U51241.1 GI:1480480  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 1717)  
AUTHORS Daugherty, B.L., Siciliano, S.J., Demartino, J.A., Malukwitz, L.,  
Siciliano, A. and Springer, M.S.  
TITLE Cloning, expression, and characterization of the human eosinophil  
eotaxin receptor  
JOURNAL J. Exp. Med. 183 (5), 2349-2354 (1996)  
MEDLINE 96235044  
PUBMED 8642344  
REFERENCE 2 (bases 1 to 1717)  
AUTHORS Daugherty, B.L.  
TITLE Direct Submission  
JOURNAL Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,  
Merck Research Laboratories, R80W-107, P.O. Box 2000, Rahway, NJ  
07065, USA  
FEATURES  
source Location/Qualifiers  
1. 1717  
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CDS 205..1272  
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YGIILKTLRCPSSKKRYKAILFVIMAVFLEFMPYNNVALISLOSITFQNDERS  
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BASE COUNT 434 a 428 c 351 g 504 t  
ORIGIN



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722 ATCTTTTATATAATCTCTGCTGACAAATGACAGGTAACCTGGCCATTGTCATGCTGTGTT 781  
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421 GCCCTTTCGAGCCCGGAGCTGCACTTTTGGTGTCAACAGACATGCTGCACTGGGGCTG 480  
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782 GCCCTTTCGAGCCCGGAGCTGCACTTTTGGTGTCAACAGACATGCTGCACTGGGGCTG 841  
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481 GCAGTCTGACGAGCTTCTGTAATTTATCTTCTATGACACATGAGAGTTGTTGAAGAG 540  
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541 ACTCTTTCGAGTCTCTTATACCCAGAGATAGATATAGCTGAGGCAATTTCCACACT 600  
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902 ACTCTTTCGAGTCTCTTATACCCAGAGATAGATATAGCTGAGGCAATTTCCACACT 961  
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962 CTGAGATACCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1021  
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661 GGAATATGAAAAAGCTGCTGAGGAGTGGCCAGTAAAAAAGTAAAGGCAATGCGGCTG 720  
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1022 GGAATATGAAAAAGCTGCTGAGGAGTGGCCAGTAAAAAAGTAAAGGCAATGCGGCTG 1081  
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721 ATTTTTCATCATGAGCGGTGTTTTCATTTTCTGAGACACCTTACATGCTGCTATCTT 780  
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1082 ATTTTTCATCATGAGCGGTGTTTTCATTTTCTGAGACACCTTACATGCTGCTATCTT 1141  
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1142 CTCTCTTCTATCATCTTATTTTGAATAGCTGTGAGCGGAGCAAGCATCTGAGAC 1201  
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841 CTGAGTATGCTGCTGAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
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1202 CTGAGTATGCTGCTGAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1261  
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901 TACGCTTTTGTGAGAGAGTTCCGGAAGTACCTGCGGCACCTTCTCCACAGAGCACTTG 960  
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1262 TACGCTTTTGTGAGAGAGTTCCGGAAGTACCTGCGGCACCTTCTCCACAGAGCACTTG 1321  
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961 CTGATGCACTGGGCAAGATACATCCATTCCTTCTGAGAGAGTGGAAAGACACAG 1020  
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1322 CTGATGCACTGGGCAAGATACATCCATTCCTTCTGAGAGAGTGGAAAGACACAG 1381  
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1021 TCGTCTTCATCCACAGAGAGCGGGAAGTCTGATTTGTTT 1065  
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1382 TCGTCTTCATCCACAGAGAGCGGGAAGTCTGATTTGTTT 1426  
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RESULT 8  
AF247361 5791 bp DNA linear PRI 26-JUN-2002  
LOCUS AF247361  
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.  
ACCESSION AF247361.1 GI:19110542  
VERSION  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
Vijh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and  
Michael,N.L.  
TITLE  
Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
for a Rare TATA-Less Promoter Structure Conserved between  
Drosophila and Humans  
JOURNAL  
MEDLINE 22074933  
GENOMICS 80 (1), 86-95 (2002)  
PUBMED 12079287  
2 (bases 1 to 5791)  
Vijh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
Direct Submission  
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.

FEATURES  
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location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 8.6e-277;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 GGCCTGCTGTGAAAAAGCTGATACCAAGACACTATGCGCCAGTTTGGCCCGCTG 120  
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DB 4075 GGCCTGCTGTGAAAAAGCTGATACCAAGACACTATGCGCCAGTTTGGCCCGCTG 4134  
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QY 361 ANCTTTTTCATATAATCTGCTGACAAATGACAGGTAACCTGGCCATTGTCATGCTGTGTT 420  
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RESULT 9
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LOCUS AC104439 Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.
DEFINITION AC104439 AC024739
ACCESSION AC104439.2 GI:21490240
VERSION HTG.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 197279)
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E.D.
TITLE Direct Submission
JOURNAL 2 (bases 1 to 197279)
AUTHORS Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 197279)
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E.D.

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# TITLE JOURNAL COMMENT

Direct Submission  
Submitted (20-JUN-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
On Jun 20, 2002 this sequence version replaced gi:117488621.

Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: <http://www.genome.washington.edu>  
Contact: uwgchgs@u.washington.edu  
Drafting team: MWGSC

Project Information  
Center project name: chr-3  
Center clone name: RP11-793E15 (bc0564)

Summary Statistics  
Sequencing vector: unknown: 5% of reads  
Sequencing vector: plasmid: 108752: 48% of reads  
Chemistry: Dye terminator ET, 94% of reads  
Chemistry: Dye terminator B1g Dye: 6% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 197168 bases at least Q40  
Consensus quality: 197255 bases at least Q30  
Consensus quality: 197275 bases at least Q20  
Insert size: 197279; sum-of-contigs  
Quality coverage: 8.2x in Q20 bases; sum-of-contigs

Overlapping Sequences:  
5': RP11-91E8 (UWGC:bc0216) AC026349  
3': CMD-2563A18 (UWGC:bc0730)

Sequence Quality Assessment:  
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

## Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII

BglIII

EcoRI

SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt
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2738	2763	10705	10502	1078	1093
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Query Match 100.0%; Score 1065; DB 9; Length 197279;  
Best Local Similarity 100.0%; Pred. No.1.3e-276;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GGCCTCTCTGTGTAAAGTGTATACAGAGCATATGGCCCAAGTTTGGCCCGCTG	120
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QY	121	TACTCCCTGTTCACCTGTGGGCTCTTGGCAATGTGGTGGTATGATCTCATTA	180
DB	190308	TACTCCCTGTTCACCTGTGGGCTCTTGGCAATGTGGTGGTATGATCTCATTA	190367
QY	181	AAATACAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTGCGAC	240
DB	190368	AAATACAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTGCGAC	190427
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DB	190428	CTGCTCTCTCTGTCACCTTCATCTGTGATCCACTATGTACGGGGGCTTAACCTGGTT	190487
QY	301	TTTGGCCATGGCATGTGTAACTCTCTCAGGGTTTATACACAGAGCTTGTACAGGAG	360
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QY	361	ATCTTTTTCATTAATCTCTGTGACAAATCGACAGGTACCTGGCCATTTGCAATGCTGTGTT	420
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QY	421	GGCCTTCGAGCCCGGACGTGACATTTTGGTGTATACACAGCATCTGTACCTGGGCGCTG	480
DB	190608	GGCCTTCGAGCCCGGACGTGACATTTTGGTGTATACACAGCATCTGTACCTGGGCGCTG	190667
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Best Local Similarity 100.0%; Pred. No. 1.3e-276;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 CTGCTCTTCCTGTCACCTCTCATCTGTGATCTGATGTCAGGGGGCACTACCTGGGT 300  
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DB 140504 CTGCTCTTCCTGTCACCTCTCATCTGTGATCTGATGTCAGGGGGCACTACCTGGGT 140563  
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QY 301 TTGGCCATGGCATGTGTAACTCTCTCAGAGTTTATACACAGAGCTTGTACAGCGAG 360  
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QY 361 ATCTTTTCAATAATCTCTGCTGACATCGACAGGTACCTGGCCATTTCCATGCTGTTT 420  
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QY 421 GCCCTCGAGCCCGGAGCTGTCACTTTTGTGTATACACAGAGCTTGTGAGCGCTG 480  
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DB 140684 GCCCTCGAGCCCGGAGCTGTCACTTTTGTGTATACACAGAGCTTGTGAGCGCTG 140743  
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QY 601 CTGAGATGAGCATCTTGTGTCTGTTCTGCCCTGCTGCTTATGAGCACTCTCTACACA 660  
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DB 140864 CTGAGATGAGCATCTTGTGTCTGTTCTGCCCTGCTGCTTATGAGCACTCTCTACACA 140923  
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QY 661 GGAATCATCAAAAGCTGCTGAGGTGCCAGTAAAAAAAAGTACAAGGCATCCGGCTC 720  
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DB 140924 GGAATCATCAAAAGCTGCTGAGGTGCCAGTAAAAAAAAGTACAAGGCATCCGGCTC 140983  
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QY 721 ATTTTGTCTCATCTGGCGGTGTTTTCATTTTGTGACACCTCTACATGTGGCTATCTT 780  
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QY 781 CTCTCTTCATCATCATCTTATTTGAAATGAGCTGAGGGGAGCAAGCATCTGGAC 840  
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LOCUS  
DEFINITION Sequence 474 from Patent WO0177172.  
ACCESSION AX280851  
VERSION AX280851.1 GI:16608181  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.  
Non-endogenous, constitutively activated known g protein-coupled  
receptors  
Patent: WO 0177172-A 474 18-0CT-2001;  
Arena Pharmaceuticals, Inc. (US)  
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Location/Qualifiers  
BASE COUNT 232 a 288 c 244 g 304 t  
ORIGIN

Query Match 99.7%; Score 1061.8; DB 6; Length 1068;  
Best Local Similarity 99.8%; Pred. No. 5.2e-276;  
Matches 1063; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 361 ATCTTTTCAATAATCTCTGCTGACATCGACAGGTACCTGGCCATTTCCATGCTGTTT 420  
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DB 361 ATCTTTTCAATAATCTCTGCTGACATCGACAGGTACCTGGCCATTTCCATGCTGTTT 420  
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QY 421 GCCCTTGAGCCCGAGCTGTCACTTTTGTGTGATCAGCAGCATCGTACCTGGGCGCTG 480  
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Db 481 GCAGTGTACAGCTCTCTCTGAAATTTATCTGTATAGAGCTGAAGGTTGTTGAAGAG 540  
QY 541 ACCTTTGAGCTGCTCTTTTACCCAGAGATACAGTATATAGCTGGAGCATTTCCACACT 600  
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Db 541 ACCTTTGAGCTGCTCTTTTACCCAGAGATACAGTATATAGCTGGAGCATTTCCACACT 600  
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RESULT 12  
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DEFINITION Sequence 2 from Patent WO0192520.  
ACCESSION AX323054  
VERSION AX323054.1 GI:18093940  
KEYWORDS  
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ORGANISM Homo sapiens  
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REFERENCE 1  
AUTHORS Barnes,A.A., Fraser,N.J., O'Shaughnessy,C.T. and Wise,A.G.  
TITLE Modified chemokine receptor ccr-3 and assay  
JOURNAL Patent: WO 0192520-A 2 06-DEC-2001;  
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ACCESSION U49727  
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REFERENCE 1 (bases 1 to 1689) Post,T.W., Wang,J., Wu,L., Gerard,N.P.,  
AUTHORS Neuman,W., Gerard,C. and Mackay,C.R.  
TITLE Molecular cloning and characterization of a human eotaxin receptor  
JOURNAL expressed selectively on eosinophils  
MEDLINE J. Exp. Med. 183 (6), 2437-2448 (1996)  
PUBMED 8676064  
REFERENCE 2 (bases 1 to 1689)  
AUTHORS Ponath,P.D.  
TITLE Direct Submission  
JOURNAL Submitted (21-FEB-1996) Paul D. Ponath, Molecular Biology,  
Leuonoste, Inc., 215 First St., Cambridge, MA 02118, USA  
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Mammalia: Eutheria; Primates; Catarrhini; Hominoidea: Homo.  
AUTHORS Kato, H., Tsuchiya, N., Izumi, S., Miyamasu, M., Nakajima, T.,  
Kawasaki, H., Hirai, K. and Tokunaga, K.  
TITLE New variations of human CC-chemokine receptors CCR3 and CCR4  
JOURNAL Genes Immun. 1 (2), 97-104 (1999)  
MEDLINE 21040311  
REFERENCE 2 (bases 1 to 1068)  
AUTHORS Kato, H., Tsuchiya, N. and Tokunaga, K.  
TITLE Direct Submission  
JOURNAL Submitted (19-FEB-1999) Hitoshi Kato, University of Tokyo,  
Department of Human Genetics, 7-3-1 Hongo, Bunkyo-ku, Tokyo  
113-0033, Japan (E-mail: kato@em.u-tokyo.ac.jp, Tel: 81-3-5841-3542,  
Fax: 81-3-5802-8619)  
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
Sol, N., Treboute, C., Gomes, E., Ferchal, F., Shacklett, B. and  
Alizon, M.  
TITLE The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor  
JOURNAL Submitted (12-JUN-1997) M. Alizon, Institut Cochin de Genetique  
Moleculaire, ICGM, 22 rue Mechain, 75014 Paris, FRANCE  
MEDLINE 9454694  
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REFERENCE 2 (bases 1 to 1068)  
AUTHORS Alizon, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-1997) M. Alizon, Institut Cochin de Genetique  
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